GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd..

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ficsult.
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Maximum Match 100%
Listing first 45 s
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Maximum DB seq length: 2000000000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Title:
Perfect score:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence:
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                                                                                                                                                                                                                                                                                                                                                                                                                                Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                            Score
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1: /SIDS1/gcgdata/
                                                                                                                                                                                                                                                                                                      Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1. \SIDSJ/gcgdata/hold-geneseq/geneseqp-embl/AA1980.DAT:*
2. \SIDSJ/gcgdata/hold-geneseq/geneseqp-embl/AA1981.DAT:*
3. \SIDSJ/gcgdata/hold-geneseq/geneseqp-embl/AA1981.DAT:*
4. \SIDSJ/gcgdata/hold-geneseq/geneseqp-embl/AA1983.DAT:*
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Gapop 10.0 , Gapext 0.
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169
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Human RSV A subtyp
Human RSV A subtyp
Human RSV A subtyp
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Amino acid sequenc	AAB68016	22	101	94.7	160	'n
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a	6774	22		٠.	σ <sub>0</sub>	ü
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tide which ind	AAW97310	20	101	94.7	σ	۵
G protein	07	20	0	٠	σ	
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V subgp. A prot	561	17	0		g	37
subgroup	825	16	0	4.	9	36
ino acid:	8414	22	13	4	9	5
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рiг	9	17	61	94.7	σ	ü
acid	8414	22	59	4	σ	
3 prote	4410	20	59	94.7	9	3
rat	9707	17	59	4	9	
acid	8414	22	57		9	
G protein ant	4410	20	57		9	82
piratory	707	17	57	94.7	9	
Amino acid sequenc	84	22	55		9	
G protein	0	20	55		160	5
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meric human r	044	10	681	96.4	163	ω
HRSV glycoprotein	AAW47605	19	298	96.4	σ	2

## ALIGNMENTS

RESULT AAW39247

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AAW3921
ID AAW39
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             antibody; Pneumovirus; identification;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAW39245 standard; peptide; 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
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                                                                            Peptide(s) derived from specific region of respiratory syncytial virus G protein - used to treat, prevent, diagnose and immunise against Pneumovirus infection
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                         Example 4;
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28..34
42
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100.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "C-terminal amide"
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Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; DB 19;
. 7.8e-16;
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RESULT
AAW39217
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Best Local
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                           AAW39217-W39234 are fragments of the human respiratory syncytial virus (RSV) G protein corresponding to amino acids 149 to 197. These fragments can be used to treat, prevent or diagnose Pneumovirus, specifically RSV, infection and to immunise against such infections. Antibodies raised from these fragments may also be used diagnostically. The fragments may also be used to identify compounds able to inhibit binding of RSV to host cells and for characterisation of cell receptors for Pneumoviruses. When the fragments are used in combination with existing vaccines, they may allow a reduction in dose, and thus side effects, of the vaccine.
                                                                                                                                                                                                              Peptide(s) derived from specific virus G protein - used to treat, against Pneumovirus infection
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      G protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
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                                                                                                                                                                               Claim 5; Fig 2; 75pp; English.
                                                                                                                                                                                                                                                                                                           Gorman
                                                                                                                                                                                                                                                                                                                                                                       05-JUN-1996;
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28; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                42 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     subtype G protein fragment (aa. 149-157) strain A2
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Pred. No.
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Length

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RESULT
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RESULT
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                                                                                                                                                                                                                                                                                                                                                     Peptide(s) derived from specific region of respiratory syncytial virus G protein - used to treat, prevent, diagnose and immunise against Pneumovirus infection
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Disulfide-bond
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100.0%; Pr
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100.0%; Pred. No. 1
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Disulfide-bond
                         antibody; Pneumovirus;
                                       G protein;
                                                                    Human RSV G protein fragment (aa. 149-157) derivative #1
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                         treatment; prevention; diagnosis; infection; immunity;
Pneumovirus; identification; vaccine; cell receptor.
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Human respiratory syncytial virus

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Best Local S
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Modified-site
                                                                                                                                                                                                                                                                               G protein; treatment;
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                                                                                                                                                                                                   Human respiratory syncytial virus
                                                                                                                                                                                                                                                        antibody; Pneumovirus;
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                                                                                                                                Modified-site
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 peptide;
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                                                                                                                                                                                                                                                                             prevention; diagnosis;
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  "C-terminal amide"
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                                                                                                                                                                                                                                                        identification;
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Pred. No.
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Matches 28
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                                                                                                                Disulfide-bond
Disulfide-bond
                                                                                                                                                                                                           antibody;
                                                                                                                                                                                                                      G protein;
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                                                                                                                                                                                   Human respiratory syncytial virus.
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Pred. No. 1.3e-1
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Best Local S
Matches 28
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Disulfide-bond
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antibody; P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       virus G protein - used to trea
against Pneumovirus infection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Peptide(s) derived from specific region of respiratory syncytial virus G protein - used to treat, prevent, diagnose and immunise
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 1998-042117/04
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Corman JJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (BIOM-) BIOMOLECULAR RES
                                                                                                                                                                                                                                                                                                     Human respiratory syncytial virus
                                                                                                                                                                                                                                                                                                                                                                   Human RSV G protein fragment (aa. 149-157) derivative #8
                                                                                                                                                                                                                                                                                                                                                                                               27-AUG-1998
                                                                                                                                                     11-DEC-1997
                                                                                                                                                                                                                                                                               Key
                                                                                                   05-JUN-1996;
                                                                                                                            04-JUN-1997;
                                                                                                                                                                             WO9746581-A1
                                                                                                                                                                                                                                                                  Modified-site
Peptide(s) derived from
                          WPI; 1998-042117/04
                                                                          (BIOM-) BIOMOLECULAR RES INST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ᆫ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          KQRQNKPPSKPNNDFHFEVFNFVPCSIC 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               l Similarity
28; Conser
                                                                                                                                                                                                                                                                                                                               ; treatment; prevention; diagnosis;
Pneumovirus; identification; vaccin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              49 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             96.4%; Score 163; llarity 100.0%; Pred. No. Conservative 0; Mismatch
                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                   96AU-0000265
                                                                                                                            97WO-AU00351
                                                                                                                                                                                                                             /note=
25..38
28..34
                                                                                                                                                                                                                                                                             Location/Qualifiers
                                                                                                                                                                                                     /note=
                                                                                                                                                                                                     "C-terminal amide"
                                                                                                                                                                                                                                                     "N-terminal biot group"
specific region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DT_{1}
                                                                                                                                                                                                                                                                                                                                                                                                                                                 AΑ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB
1
                                                                                                                                                                                                                                                                                                                               vaccine; cell receptor
of respiratory syncytial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 19;
l.3e-15;
                                                                                                                                                                                                                                                                                                                                            infection; immunity;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 49;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0;
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RESULT 10
AAP70845
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 δõ
Query Match
Best Local Similarity
Matches 28; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAW39244-W39252 are derivatives of the human respiratory syncytial virus (RSV) G protein corresponding to amino acids 149 to 197. These fragments can be used to treat, prevent or diagnose Pneumovirus, specifically RSV, infection and to immunise against such infections. Antibodies raised from these fragments may also be used diagnostically. The fragments may also be used to identify compounds able to inhibit binding of RSV to host cells and for characterisation of cell receptors for Pneumoviruses. When the fragments are used in combination with existing vaccines, they may allow a reduction in dose, and thus side effects, of the vaccine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               virus {\tt G} protein - used to treat, prevent, diagnose and immunise against Pneumovirus infection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Example 4; Fig 12; 75pp; English.
                                         A novel plasmid which comprises a DNA sequence encoding this protein, and the protein itself, are claimed, for use as HRSV vaccines. The vaccine can be administered to pregnant women or to women of child bearing age to stimulate maternal antibodies.
                                                                                                                                     Vaccines for human respiratory virus \cdot comprising proteins or fragment encoded by a DNA sequence coding for human respiratory syncytial virus proteins.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           05-APR-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAP70845;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAP70845 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                 WO8704185-A.
                                                                                                                                                                                                                                                                                                                                                                                                          Human respiratory syncytial virus (HRSV)
                                                                                                                                                                                                                                                                                                                                                                                                                                        Vaccine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence of
                                                                                                            Disclosure; Chart 13; 57pp;
                                                                                                                                                                                                N-PSDB;
                                                                                                                                                                                                                                    (UYNC-) UNIV OF N CAROLINA (WERT/) WERTZ G W. (WERT/) WERTZ G W.
                                                                                                                                                                                                                                                                                              14-JAN-1986;
                                                                                                                                                                                                                                                                                                                          23-DEC-1986;
Sequence
                                                                                                                                                                                                                                                                                                                                                     16-JUL-1987
                           Infants
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1987-206300/29
DB; AAN70784.
                           can also be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  49
 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              human respiratory syncytial virus (HRSV) A2 strain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             96.4%;
ilarity 100.0%;
Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AA;
 A
                                                                                                                                                                                                                                                                                               86US-0818740
                                                                                                                                                                                                                                                                                                                          86WO-US02756
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           entry)
                             vaccinated at 2-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 163; DB 19; Pred. No. 1.3e-10; Mismatches
                                                                                                               English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    28
                              months
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          19;
                              of.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 49;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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0

Query Match

96.4%;

Score 163;

DB

8,

Length 298;

G; gpG; vaccine

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RESULT 12
AAW47505
ID 4AW4761
XX AAW4761
AC AAW4761
XX DT 11-JUN
XX DE HRSV 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 1
AAR25302
ID AAR2
                                                                                                                                                                         B
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                                                                                               D,
                                                                                                              S
                                                                                                                              Query Match
Best Local S
Matches 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity Matches 28; Conserv
                                                                                                                                                                                      The sequences of mRNA encoding HRSV structural proteins are given in AAQ29672-26. The proteins are F, G, 22K, 9,5K and major capsid protein N. The sequences and encoded proteins are useful for preparing vaccines against HRSV. The vaccines can be used to conferimmunity against respiratory tract infections on human subjects.
                                                                                                                                                                                                                                                                                                                                                                                                        US5149650-A
                                                                                                                                                                                                                                                                                                                                                                                                                                       Vaccine; human respiratory major capsid protein; N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 03-MAR-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAR25302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAR25302 standard;
                                                                                                                                                                                                                                        Disclosure; Page 18; 21pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                       Human respiratory syncytial virus strain A2
       HRSV glycoprotein
                        11-JUN-1998
                                                        AAW47605 standard;
                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                               Vaccines for human respiratory virus - include structural genes coding for native structural viral proteins and immunogenic
                                                                                                                                                                                                                                                                                          N-PSDB;
                                                                                                                                                                                                                                                                                                                Collins PL,
                                                                                                                                                                                                                                                                                                                                                                       14-JAN-1986;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               HSRV glycoprotein G
                                                                                                                                                                                                                                                                                                                                (UYNC-) UNIV NORTH CAROLINA
                                                                                                                                                                                                                                                                                                                                               14-JAN-1986;
13-JUL-1988;
                                                                                                                                                                                                                                                                                                                                                                                         22-SEP-1992
                                                                                                149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       149 kgrqnkppskpnndfhfevfnfvpcsic 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               11
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                                                                                                                KQRQNKPPSKPNNDFHFEVFNFVPCSIC 28
                                                                                                                                                                                                                                                                                        1992-340247/41.
DB; AAQ29623.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KORONKPPSKENNDFHFEVFNFVPCSIC 28
                                                                                               kgrgnkppskpnndfhfevfnfvpcsic 176
                                                                                                                                28; Conservative
                                                                                                                                                                         298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                        (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                                                                                                                                                                Wertz GW;
                                                                                                                                                                         AA.
                                                                                                                                                                                                                                                                                                                                               86US-0818740
88US-0218737
                                                                                                                                                                                                                                                                                                                                                                       86US-0818740
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Protein;
                                                        Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               (gpG).
                                                                                                                                      96.48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                               syncytial virus; HRSV;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0
                                                        298
                                                                                                                                0
                                                                                                                                      Score 163; DB 13
Pred No. 8.6e-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pred. No. 8.6e-15;
Mismatches 0;
                                                        Ą
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Å
                                                                                                                               Mismatches
                                                                                                                                                DB 13;
                                                                                                                                               Length 298;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 ''J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                 <u>د</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                 22K;
                                                                                                                                0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0
                                                                                                                                                                                                                                                                                                                                                                                                                                                 9.5K
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0;
                                                                                                                                0
                                                                                                                                                                                      RESULT 13
AAP90441
                                                                                                                                                                                                                                                                                                В
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                                                                                                                                                                                                                                                                Query Match
Best Local
                                                                                                                                                                                                                                                        Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              13-JUL-1988;
14-JAN-1986;
23-DEC-1986;
11-JUN-1992;
12-MAY-1997;
                                                  29-JUN-1989.
                                                                                                     Chimeric polypeptide; protein F; protein G:
                                                                                                                                               01-NOV-1989
                                                                                                                                                               AAP90441;
                                                                                                                                                                                AAP90441 standard;
                                                                                                                                                                                                                                                                                                Sequence
                                                                                                                                                                                                                                                                                                                                                                                        DNA
                                                                                                                                                                                                                                                                                                                                                                                                                        N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                Collins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US5716823-A.
                       23-DEC-1987;
                                      31-OCT-1988;
                                                                       WO8905823-A
                                                                                                                                                                                                                                                                                                                                                                                                                                WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               (PHAA ) PHARMACIA & UPJOHN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               12-MAY-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                10-FEB-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HRSV; glycoprotein F; gpF; glycoprotein
      (UPJO ) UPJOHN
                                                                                                                                                                                                                                                                                                                                                                                                                       1998-144802/13.
DB; AAV18736.
                                                                                                                                                                                                                                                                                                                                                                                                                                               PL,
                                                                                                                                                                                                                                                      Similarity 100.
28; Conservative
                                                                                                                                                                                                                                                                                                298 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                               Wertz GW;
                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              88US-0218737.
86US-0818740.
86WO-US02756.
92US-0897171.
97US-0854783.
                       87US-0137387
                                      88WO-US03784
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               97US-0854783
                                                                                                                                                                                protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               CO
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The present sequence was used in the development of a novel method for the production of human respiratory syncytial virus (HRSV) glycoprotein F (gpF) or glycoprotein G (gpG). The method comprises culturing eukaryotic host cells transfected with an isolated DNA sequence encoding HRSV gpF or gpG. The gp can be used to prepare vaccines against HRSV.
                                                                                                                                       Chimeric human respiratory synctial virus glycoproteins F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Production of human respiratory syncytial virus glyco-protein F or G by culturing eukaryotic host cells transfected with corresponding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human respiratory syncytial virus
Human respiratory syncytial virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Example 1; Columns 27-28; 17pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                            1 KQRQNKPPSKPNNDFHFEVFNFVPCSIC 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          96.4%; Score 163; DI
100.0%; Pred. No. 8.0
Live 0; Mismatches
                                                      human respiratory vaccine.
                                                                                                                                                                                                                                                                                                           189
                                                                                                                                                                                                                                                                                                           ΑA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 19;
8.6e-15;
                                                                                syncytial virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 298;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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RESULT 1
AAW39218
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           immunogenic fragments from both human respiratory glycoproteins F and G. Can be used in vaccines. E. coli, Chinese hamster ovary cells, murine C127 S. frugiperda.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  contg.f and G,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Chimeric
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Wathen M;
                                                                                                                                                                                                                                                                                                                                                                                                  Human RSV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAW39218 standard;
                                                                                                                                                                                                                                                                                                  Disulfide-bond
Disulfide-bond
                                                                                                                                                                                                                                                                                                                                              Human
                                                                                                                                                                                                                                                                                                                                                                                                                         27 - AUG - 1998
                                                                                                                                                                                                                                                                                                                                                                                                                                             AAW39218
AAW39217-W39234 are fragments of the human respiratory syncytial virus (RSV) G protein corresponding to amino acids 149 to 197. These fragments can be used to treat, prevent or diagnose Pneumovirus, specifically RSV, infection and to immunise against such infections. Antibodies raised from these fragments may also be used diagnostically. The fragments may also be used to inhibit binding of RSV to
                                                                                                Peptide(s) derived from specific virus G protein - used to treat, against Pneumovirus infection
                                                                                                                                                                                                             05-JUN-1996;
                                                                                                                                                                                                                                 04-JUN-1997;
                                                                                                                                                                                                                                                       11-DEC-1997
                                                                                                                                                                                                                                                                            WO9746581-A1
                                                                                                                                             WPI; 1998-042117/04
                                                                                                                                                                                       (BIOM-) BIOMOLECULAR
                                                                            Claim 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        543
                                                                                                                                                                                                                                                                                                                                                                             protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity
les 28; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 KORONKPPSKPNNDFHFEVFNFVPCSIC 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1989-206593/28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     kgrqnkppskpnndfhfevfnfvpcsic 570
                                                                                                                                                                                                                                                                                                                                            respiratory syncytial virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 human respiratory syncytial virus polypeptides(s) immunogenic fragments from HRSV glycoproteins for vaccine prodn.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             page 47-48;
                                                                           Fig
                                                                                                                                                                                                                                                                                                                                                                                                  A subtype G
                                                                                                                                                                                                                                                                                                                                                                   Pneumovirus;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          681 AA;
                                                                                                                                                                                                                                                                                                                                                                            treatment; prevention; diagnosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                            2;
                                                                                                                                                                                                                                 97WO-AU00351
                                                                                                                                                                                                             96AU-0000265
                                                                          75pp;
                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  peptide; 49 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              96.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            50pp;
                                                                                                                                                                                       RES INST
                                                                                                                                                                                                                                                                                                                                                                                                  protein fragment (aa 149-157) strain long
                                                                            English
                                                                                                                                                                                                                                                                                                                                                                    identification;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               English,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 163;
Pred. No.
                                                                                                                                                                                        LTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
                                                                                                          region of respiratory syncytial prevent, diagnose and immunise
                                                                                                                                                                                                                                                                                                                                                                    vaccine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2e-14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 10;
                                                                                                                                                                                                                                                                                                                                                                               infection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          d one or more
/ syncytial virus
Hosts are, eg
/ cells and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 681;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                             immunity;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0
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KQRQNKPPSKPNNDFHFEVFNFVPCSIC

28

0

Indels

0

Gaps

0

27; Conservative

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RESULT
AAW39221
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                                                             В
Query Match
Best Local S
Matches 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
                                                                                                                    AAW39217-W39234 are fragments of the human respiratory syncytial virus (RSV) G protein corresponding to amino acids 149 to 197. These fragment can be used to treat, prevent or diagnose Pneumovirus, specifically RSV infection and to immunise against such infections. Antibodies raised from these fragments may also be used diagnostically. The fragments may also be used to inhibit binding of RSV to also be used to identify compounds able to inhibit binding of RSV to
                                                                                                                                                                                                                                                                                                                                                                                   04-JUN-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Disulfide-bond
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Disulfide-bond
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Key
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human respiratory syncytial virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            27-AUG-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAW39221;
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                                                                                                                                                                                                          Claim 5; Fig 2;
                                                                                                                                                                                                                                 Peptide(s) derived from specific region of respiratory virus G protein - used to treat, prevent, diagnose and against Pneumovirus infection
                                                                                                                                                                                                                                                                                   WPI; 1998-042117/04
                                                                                                                                                                                                                                                                                                           Gorman
                                                                                                                                                                                                                                                                                                                                                          05-JUN-1996;
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                                                           Sequence
                                                                                 host cells and for characterisation of cell receptors for Pneumoviruses. When the fragments are used in combination with existing vaccines, they may allow a reduction in dose, and thus side effects, of the vaccine.
                                                                                                                                                                                                                                                                                                                                 (BIOM-) BIOMOLECULAR RES INST LTD
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Search completed: September 4, 2002, 17:36:21 Job time: 255 sec

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Compugen Ltd
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(without alignments)
188.793 Million cell updates/sec
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45	44	43	42	41	40	39	38	37	36	35 5	34	33	32	31	30
47	47	47	47	47.5	47.5	48	48	48	48	48.5	49	49.5	50	50	50
27.8	27.8	27.8	27.8	28.1	28.1	28.4	28.4	28.4	28.4	28.7	29.0	29.3	29.6	29.6	29.6
455	388	212	113	895	289	846	661	513	340	633	419	104	398	290	96
2	N	N	N	N	N	ν	N	N	N	N	Ν	Ν	N	2	Ν
JC1224	T32994	G69838	S43435	T45738	AH2478	F75525	A58768	T30733	F85256	T47524	D86453	G84607	D81397	G82360	H84381
nucleobindin	hypothetical	hypothetical	nuclear receptor	hypothetical prote	transposase all700	outer membrane pro	ATP-dependent RNA	A-type inclusion	hypothetical prote	hypothetical prot	CDS protein F9L11	hypothetical prote	probable periplasm	diaminopimelate ep	hypothetical prote

## ALIGNMENTS

RESULT

attachment protein - human respiratory syncytial virus (strain RSB1734)
N;Alternate names: G protein
C;Species: human respiratory syncytial virus
C;Date: 31-Mar-1992 #sequence\_revision 31-Mar-1992 #text\_change 16-Feb-1997
C;Accession: JQ1205
R;Cane, P.A.; Matthews, D.A.; Pringle, C.R.
J. Gen. Virol. 72, 2091-2096, 1991-A;Reference number: JQ1204; MUID:91374005
A;Accession: JQ1205

A; Molecule type: mrNA
A; Residues: 1-297 <CAN>
C; Comment: Respiratory syncytial virus commonly causes severe lower respiratory tractilidren and adults.

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R:Cane, P.A.; Matthews, D.A.; Pringle, C.R.
J. Gen. Virol. 72, 2091-2096, 1991
A;Title: Identification of variable domains of the attachment (G) protein of subgroup A;Reference number: JQ1204; MUID:91374005
A;Accession: JQ1204
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Residues: 1-297 <CAND
C;Comment: Respiratory syncytial virus commonly causes severe lower respiratory tract
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C;Superfamily: respiratory syncytial virus major surface glycoprotein G
C;Keywords: glycoprotein; transmembrane protein
F;85,103,135,237,251,273/Binding site: carbohydrate (Asn) (covalent) #status predicte
                                                              C;Superfamily: respiratory syncytial virus major surface glycoprotein C;Keywords: glycoprotein; transmembrane protein F;85,103,135,144,237,273/Binding site: carbohydrate (Asn) (covalent)
                                                                                                                                                                                                                                                                                                                                  N;Alternate names: G protein
C;Species: human respiratory syncytial virus
C;Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 16-Feb-1997
C;Accession: JQ1204
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hes 28; Conservative
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100.0%;
    96.48;
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1991
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  Score 163;
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major surface glycoprotein G - human respiratory syncytial virus
C:Species: human respiratory syncytial virus
C:Species: human respiratory syncytial virus
C:Date: 28-May-1986 #sequence_revision 28-May-1986 #text_change 24-Sep-1999.
C:Accession: A94048; A93599; A04039
R:Wertz, G.W.: Collins, P.L.; Huang, Y.: Gruber, C.: Levine, S.; Ball, L.A.
Proc. Natl, Acad. Sci. U.S.A. 82, 4075-4079, 1985
A:Title: Nucleotide sequence of the G protein gene of human respiratory syncytial virus
A:Reference number: A94048; MUID:85216636
A:Accession: A94048
A:Residues: 1-98 <WER>
A:Cross-references: GB:M1486; GB:K01459; GB:K02719; GB:K03348; GB:K03349; GB:M11217; GB
A:Note: residues 207-298 are identical with residues 376-467 of the nucleocapsid protein
A:Note: residues 207-298 are identical with residues 376-467 of the nucleocapsid protein
A:Note: this protein may carry 40-80 separate O-linked carbohydrate chains distributed a
R:Satake, M.; Coligan, J.E.; Elango, N.; Norrby, E.; Venkatesan, S.
Nucleic Acids Res. 13, 7795-7812, 1985
A:Accession: A93599; MUID:86067198
A:Accession: A93599; MUID:86067198
A:Accession: A93599; MUID:86067198
A:Residues: 1-98 <SAT>
A:Cross-references: GB:X03149; NID:g60997; PIDN:CAA26928.1; PID:g60998
C:Keywords: glycoprotein; transmembrane protein
F:38-65/Domain: transmembrane status predicted <TNM>
F:85.135,237,251/Binding site: carbohydrate (Asn) (covalent) #status predicted

R:Status predicted <TNM>
F:85.135,237,251/Binding site: carbohydrate (Asn) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                         attachment protein - human respiratory syncytial virus N;Alternate names: G protein C;Species: human respiratory syncytial virus C;Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #tex C;Accession: JQ1208 R;Cane, P.A.; Matthews, D.A.; Pringle, C.R. J. Gen. Virol. 72, 2091-2096, 1991 A;Title: Identification of variable domains of the atta A;Reference number: JQ1204; MUID:91374005 A;Accession: JQ1208
                                                                                                                                                                                                                                                   A:Molecule type: mRNA
A:Residues: 1-297 <CAN>
C:Comment: Respiratory syncytial virus commonly causes
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                                                                                                                                                                                                                             ildren and adults.
                                                                                                                                            ;Superfamily: respiratory syncytial virus major surface glycoprotein G;Keywords: glycoprotein; transmembrane protein
;Reywords: glycoprotein; transmembrane protein
;85,103,135,237,251,273,294/Binding site: carbohydrate (Asn) (covalent)
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Best Local Similarity
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                     Query Match
Best Local Similarity
Matches 27: Conserv
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                                             Score 160; DB 2;
Pred. No. 8.3e-15;
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                                                                      Length 297;
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                                                                                                                                                                                                                                                        severe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (strain RSB6256)
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RESULT
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A;Cross-references: GB:M17212; NID:g333940; PIDN:AAA4741;
R;Garcia-Barreno, B.; Portela, A.; Delgado, T.; Lopez, J
R;Garcia-Barreno, B.; Portela, A.; Delgado, T.; Lopez, J
EMBO J. 9, 4181-4187, 1990
A;Title: Frame shift mutations as a novel mechanism for t
A;Reference number: S12279; MUID:91065351
A;Accession: S12279
A;Accession: S12279
A;Molecule type: mRNA
A;Residues: 1-298 <GAR>
C;Superfamily: respiratory syncytial virus major surface
C;Keywords: glycoprotein; transmembrane protein
F;41-3/Domain: transmembrane #status predicted <TMN>
F;85,103,135,179,237,250,251,273.294/Binding site: carbol
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  R:Johnson, P.R.; Spriggs, M.K.; Olmsted, R.A.; Collins, P.L. Proc. Natl. Acad. Sci. U.S.A. 84, 5625-5629, 1987
A;Title: The G glycoprotein of human respiratory syncytial viruses of subgroups A;Reference number: A32703; MUID:87289657
A;Accession: A32703
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C:Species: human respiratory syncytial virus
C:Date: 31-Mar-1991 #sequence_revision 31-Mar-1991
                                                                                                                                                                                   C;Superfamily: respiratory syncytial virus major surface glycoprotein C;Keywords: glycoprotein; transmembrane protein F;85,103,135,237,250,273,294/Binding site: carbohydrate (Asn) (covaler
                                                                                                                                                                                                                                               A; Molecule type: mRNA
A; Residues: 1-298 «CAN»
A; Note: the authors translated the codon
C; Comment: Respiratory syncytial virus co
lidren and adults
                                                                                                                                                                                                                                                                                                                                                                             R;Cane, P.A.; Matthews, D.A.; Pringle, C.R.
J. Gen. Virol. 72, 2091-2096, 1991
A;Title: Identification of variable domains
A;Reference number: JQ1204; MUID:91374005
                                                                                                                                                                                                                                                                                                                                                                                                                                                             N:Alternate names: G protein c;Species: human respiratory syncytial C;Date: 31-Mar-1992 *sequence_revision C;Accession: J01207
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A; Residues: 1-298 <JOH>
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Best Local (
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Matches 27; Conser
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                      1 KQRQNKPPSKPNNDFHFEVFNFVPCSIC 28
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KQRQNKPPNKPNNDFHFEVFNFVPCSIC 176
                                                                                                   Similarity
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                                                                                                   94.78;
                                                                               Score 160; DE
Pred. No. 8.36
1; Mismatches
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Pred. No. 8
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31-Mar-1992
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T.; Lopez, J.A.;
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.3e-15;
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severe
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Melero, J.A
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JC5680

G protein - Human respiratory syncytial virus
C:Species: Human respiratory syncytial virus
C:Species: Human respiratory syncytial virus
C:Date: 11-Nov-1997 #sequence_revision 11-Nov-1997 #text_chaic
C:Accession: JC5680
R:Geng, X: Wang, Z:; Qian, Y:; Zhu, R.; Deng, J.; Du, J.; Zi
Chinese J. Virol. 12, 317-322, 1996
A;Title: Molecular analysis of G protein gene of a respirato;
A;Reference number: JC5680
A;Accession: JC5680
C:Superfamily: respiratory syncytial virus major surface 165
C:Superfamily: respiratory syncytial virus major surface 91y
F;1-38/Domain: intracellular #status predicted <INUT>
F;1-38/Domain: transmembrane #status predicted <INUT>
F;67-298/Domain: extracellular #status predicted <INUT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ildren and adults.

C:Superfamily: respiratory syncytial virus major surface glycoprotein C:Keywords: glycoprotein; transmembrane protein C:Keywords: glycoprotein; transmembrane protein F:85,103,135,237,251,273,294/Binding site: carbohydrate (Asn) (covaler
                               N:Alternate names: G protein
:Species: human respiratory syncytial virus
:Species: human respiratory syncytial virus
C:Date: 31-Mar-1992 #sequence_revision 31-Mar-1992
C:Accession: JQ1209
R:Cane, P.A.; Matthews, D.A.; Pringle, C.R.
J. Gen. virol. 72, 2091-2096, 1991
A:Title: Identification of variable domains of the
A:Reference number: JQ1204; MUID:91374005
A:Accession: JQ1209
A:Accession: JQ1209
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JQ1209
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A; Residues: 1-297 <CAN>
C; Comment: Respiratory:
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J. Gen. Virol. 72, 2091-2096, 1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         N;Alternate names: G protein
C:Species: human respiratory syncytial virus
C:Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 16-Feb-1997
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A; Molecule type: mRNA
A; Residues: 1-297 <CAN>
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Best Local S
Matches 27
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Best Local 9
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27; Conserv
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Pred. No. 5.7e
1; Mismatches
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Pred. No. 8.3e-15;
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C;Accession: A37077
R;Sullender, W.M.; Anderson, K.; Wertz, G.W.
Virology 178, 195-203, 1990
A;Title: The respiratory syncytial virus subgroup
gous subgroup virus challenge.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Molecule type: mRNA
A;Residues: 1-292 <JOHA
A;Cross-references: GB:M17213; NID:g333942; PIDN:AAA47412.1;
A;Cross-references: GB:M17213; NID:g333942; PIDN:AAA47412.1;
C;Superfamily: respiratory syncytial virus major surface glyc
C;Keywords: glycoprotein; transmembrane protein
E;41-63/Domain: transmembrane #status predicted <TMN>
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                                                                                            C:Superfamily: respiratory syncytial virus major surface glycoprotein (Keywords: glycoprotein); transmembrane protein E;45-63/Domain: transmembrane #status predicted <TMN> E;81,86,100,230,290/Binding site: carbohydrate (Asn) (covalent) #status
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           R;Johnson, P.R.; Spriggs, M.K.; Olmsted, R.A.; Collins, P.L. proc. Natl. Acad. Sci. U.S.A. 84, 5625-5629, 1987
A;Title: The G glycoprotein of human respiratory syncytial viruses of subgroups A;Reference number: A32703; MUID:87289657
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    major surface glycoprotein G · human respiratory syncytial virus (strain 18537) C;Species: human respiratory syncytial virus C;Date: 31-Mar-1991 #sequence_revision 31-Mar-1991 #text_change 16-Jul-1999
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                                                                                                                                                                                                A; Gene:
                                                                                                                                                                                                                                      A;Molecule type: mRNA
A;Residues: 1-292 <SUL>
A;Cross-references: EMBL:M55633; NID:g333944; PIDN:AAA47413.1; PID:g333945
                                                                                                                                                                                                                                                                                                                A; Reference number: A37077; A; Accession: A37077
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C;Date:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C; Species: human respiratory syncytial virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MGNZ60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                F;81,86,100/Binding site: carbohydrate (Asn) (covalent) #status
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Accession: B32703
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                                                                                                                                                                                                                       ; Genetics:
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               149 KQHQNKPBNKPNNHFHFEVFNFVPCSIC 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         149 KSRSKNPPKKPKDDYHFEVFNFVPCSICG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 16.Jul-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 l Similarity
25; Conser
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          oprotein G - human respiratory syncytial virus (strain 8/60)
attachment glycoprotein G
76.98;
72.48;
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72.48;
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89.3%;
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1; Mismatches
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Score 130; DB 1; Pred. No. 1.3e-10;
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Pred. No. 1.3e-10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            177
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 2;
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                    Length 292;
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                                                                                                 (covalent) #status
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coprotein G
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Conservative

2,

Mismatches

Indels

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Gaps

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C:Species: Drosophila melanogaster
C:Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 17-Nov-2000
C:Accession: T13845
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(Specles: Mus musculus (house mouse)

C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 13-Jan-1995

C:Accession: S48861

R:Nehls, M.; Pfeifer, D.; Lueno, K.; Boehm, T.

submitted to the EMBL Data Library, September 1994

A:Description: A transcription map of the region flanked by betaA3-crystallin and neurof A:Reference number: S48861

A:Accession: S48861

A:Status: preliminary
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glycoprotein G - ovine respiratory syncytial virus C:Species: ovine respiratory syncytial virus C:Species: ovine respiratory syncytial virus C:Date: 28-Aug-1985 #sequence_revision 07-Oct-1994 #text_change 28-May-1999 C:Accession: JQ2388 R:Mallipeddi, S.K.; Samal, S.K.
J. Gen. Virol. 74, 2787-2791, 1993 J. A:Title: Analysis of the ovine respiratory syncytial virus (RSV) G glycoprotein gene A:Reference number: JQ2388; MUID:94103788
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A:Status: preliminary: translated from GB/EMBL/DDBJ
A:Molecule type: mRNA
A:Residues: 1-1861 <SAU>
A:Cross-references: EMBL:U95171; NID:g1930121; PID:g1930122; PIDN:AAB51540.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Reference number: A; Accession: T13845
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   R; Saunders, R.D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        microtubule-associated protein - fruit fly (Drosophila melanogaster)
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A;Residues: 1-1188 <NEH>
A;Cross-references: EMBL:X81632
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JQ2388
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Best Local Similarity 42.3
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Best Local Similarity
Matches 10; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Saunders, R.D.; Avides, M.C.; Howard, Cell Biol. 137, 881-890, 1997
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                                                                                                                                                                                                                                                                                                  410 RNMPPLKFYHDFHSEIFQYTVVWGPC 435
                                                                                                                                                                                                                                                                                                                                            4 QNKPPSKPNNDFHFEVFNFV----PC 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KQRQNKPPSKPNNDFHFEVFNFVPCSI 27
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Search completed: Job time: 132 sec

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R;Alansari, H.: Potgieter, L.N.
Virology 196, 873-877, 1993
A;Title: Nucleotide sequence analysis of the ovine respiratory syncytial virus + A:Reference number: A48732; MUID:93383418
A:Accession: A48732
A:Status: preliminary
A:Molecule type: nucleic acid
A:Residues: 1-263 <ALA>
A:Residues: 1-263 <ALA>
A:Molecules: 1-263
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A:Experimental source: WSU 83-1578
C:Superfamily: respiratory syncytial virus major surface glycoprotein G
C:Keywords: glycoprotein: transmembrane protein
F:1-37/Domain: intracellular #status predicted <TMM>
F:38-64/Domain: extracellular #status predicted <EXT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              attachment glycoprotein G - ovine respiratory syncytial virus ORSV C:Species: ovine respiratory syncytial virus C:Date: 16-Feb-1994 #sequence_revision 25-Apr-1997 #text_change 30
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Вр
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R:Alansari, H.: Pot
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A48732
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Best Local
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                                                                                       4 QNKPPSKPNNDF-HFEVFNFVPCSIC
    OKSNPSEIOODYSDFOILPYVPCNIC 176
                                                                                                                                                                              l Similarity 38.9
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Pred. No. 3;
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Pred. No. 3;
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Result
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq
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TAC1_HUMAN
NCB1_MOUSE
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PRT; 297 AA. Led) sequence update) annotation update)	CSIC 28	Score 163; DB 1; Length 297; Pred. No. 6.2e-15; , Mismatches 0; Indels 0; Gaps	O-LINKED GLCNAC.  NKED (GLCNAC.  NKED (GLCNAC.  NKED (GLCNAC.  NKED (GLCNAC.	895054; Pringle C.R.; pringle C.R.; e domains of the attachment (G) protein of cytial viruses."; f6(1991). THER PARAMYXOVIRUS ATTACHMENT PROTEINS, THE VIRUS G PROTEIN LACKS BOTH NEURAMINIDASE AND TITLES. EXPRESSED ON THE SURFACE OF THE INFECTED TATE THE FORESTER OF THE INFECTED	red) sequence update) sequence update) annotation update) G (Attachment glycoprotein G). c. virus (strain rsb642). rand viruses; Mononegavirales; nae; Pneumovirus.	PRT; 297 AA.

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"Identification of variable domains of the attachment (G) protein o subgroup A respiratory syncytial viruses.";

J. Gen. Virol. 72:2091-2096(1991).

-I- FUNCTION: UNLIKE THE OTHER PARAMYXOVIRUS ATTACHMENT PROTEINS, T. RESPIRATORY SYNCYTIAL VIRUS G PROTEIN LACKS BOTH NEURAMINIDASE;

HEMAGGLUTINATING ACTIVITIES.

-I- SUBCELLULAR LOCATION: EXPRESSED ON THE SURFACE OF THE INFECTED CELLS AND INCORPORATED IN THE MEMBRANE OF THE VIRIONS.

-I- PTM. MAY CARRY 40-80 SEPRAFE O-LINKED CARRONYDRATE CHAINS DISTRIBUTED AMONG THE 91 SERINE AND THREONINE RESIDUES.

PIR: J01205; J01205.
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                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.

MEDLINE-85216636; PubMed=3858865;

Mertz G.W., Collins P.L., Huang Y., Gruber C., Levine S., Ball L.A.;

"Nucleotide sequence of the G protein gene of human respiratory

syncytial virus reveals an unusual type of viral membrane protein.";

proc. Natl. Acad. Sci. U.S.A. 82:4075-4079(1985).
                                                                                                                                                                                                                                                                                                                                                                                                                  Viruses; ssRNA negative-strand Paramyxoviridae; Pneumovirinae; NCBI_TaxID=11259;
                                                                                                                                                                                                                                                                                                                                                                                                                                            Human respiratory syncytial virus (strain A2).
Viruses; ssRNA negative-strand viruses; Mononegavirales.
Paramyxoviridae; Pneumovirinae; Pneumovirus.
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SEQUENCE FROM N.A. MEDLINE 95266253; Connors M., Crowe
                                                                                                                                 SEQUENCE FROM N.A.
MEDLINE-86067198; PubMed-4069997;
Satake M., Coligan J.E., Elango N., No
Respiratory syncytial virus envelope
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66253; PubMed=7747420;
Crowe J.E. Jr., Fires
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"-LINKED (GLCNAC. . .) (POTENTIAL)

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InterPro: IFACO Pfam; PF00802;

PIR;

A04039; MGNZ

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EMBL; M11486; AAB59857.1; EMBL; X03149; CAA26928.1; ---
EMBL; X0362; AAB886663.1; ---
EMBL; U50363; AAB88675.1; ---
EMBL; U63644; AAC55969.1; ---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             virus con
Virology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE-97187925; PubMed-9035372; Mitchead S.S.,
                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a c between the Swiss Institute of Bioinformatics and the EMBL the European Bioinformatics Institute. There are no restrict use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and fo entitles requires a license agreement (See http://www.isb-sib.or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                         Virus
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virus contains mu
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CELLS AND INCORPORATED IN THE MEMBRANE OF THE VIRIONS.
PTM: MAY CARRY 40-80 SEPARATE O-LINKED CARBOHYDRATE CHAINS
DISTRIBUTED AMONG THE 91 SERINE AND THREONINE RESIDUES.
                                                                                                                                                                                                                                                                                                                                                                                           FUNCTION: UNLIKE THE OTHER PARAMYXOVIRUS ATT
RESPIRATORY SYNCYTIAL VIRUS G PROTEIN LACKS
HEMAGGLUTINATING ACTIVITIES.
SUBCELLULAR LOCATION: EXPRESSED ON THE SURFA
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Genes 13:269-273(1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               tion of the ts phenotype by a chemically mutagenized co human respiratory syncytial virus vaccine candidate re acquisition of a single mutation in the polymerase (L)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ntains mutations in the 208:478-484(1995).
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                   Similarity 100
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hes 0;
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CARBOHYD CARBOHYD SEQUENCE

N-LINKED (GLCNAC...)
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N-LINKED (GLCNAC...)
1 993C3D2DD68BC634 CRC6

) (POTENTIAL). ) (POTENTIAL). ) (POTENTIAL).

CRC64;

EXTRACELLULAR (POTENTIAL)

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CYTOPLASMIC

(POTENTIAL).

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149

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VGLG_HRSV6
P27025;
01-AUG-1992 (Re
01-AUG-1992 (Re
01-AUG-1992 (Re
Major surface c
SEQUENCE FROM N.A.
MEDLINE=91374005; PubMed=1895054;
Cane P.A., Matthews D.A., Pringle
                                          Viruses: ssRNA negativė-strand viruses: Mononegavirales
Paramyxoviridae: Pneumovirinae: Pneumovirus.
NCBI_TaxID=11256:
                                                                                                                                                                      HRSV6
                                                                             Human
                                                                             respiratory syncytial virus (strain rsb6256)
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2 (Rel. 23, Last seque
2 (Rel. 23, Last annotated)
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P27024;
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01-AUG-1992 (Rel. 23, Last sequence update)
30-AMY-2000 (Rel. 39, Last annotation update)
Major surface glycoprotein G (Attachment glycoprotein
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J. Gen. Virol. 72:2091-2096(1991).

- FUNCTION: UNLIKE THE OTHER PARAMYXOVIRUS ATTACHMENT PROTEINS, TRESPIRATORY SYNCYTIAL VIRUS G PROTEIN LACKS BOTH NEURAMINIDASE HEMAGGLUTINATING ACTIVITIES.

- I- SUBCELLULAR LOCATION: EXPRESSED ON THE SURFACE OF THE INFECTED CELLS AND INCORPORATED IN THE MEMBRANE OF THE VIRIONS.

- I- PTM: MAY CARRY 40-80 SEPARATE O-LINKED CARBOHYDRATE CHAINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A. MEDLINE-91374005; PubMed-1895054;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Paramyxoviridae;
NCBI_TaxID=11255;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human respiratory syncytial virus (strain rsb6190). Viruses; ssRNA negative-strand viruses; Mononegavirales;
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Pfam; PF00802; Glycoprotein_G; 1.
Transmembrane; Glycoprotein.
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pr00802; Glycoprotein_G; 1.
membrane; Glycoprotein.
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EXTRACELLULAR (POTENTIAL).

N-LINKED (GLCNAC. .) (POTENTIAL).

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N-LINKED (GLCNAC. .) (POTENTIAL).

N-LINKED (GLCNAC. .) (POTENTIAL).
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Pred. No. 1.6e-14;
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P20895;
01-FEB-1991
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CARBOHYD
CARBOHYD
CARBOHYD
CARBOHYD
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                          antigenically related proteins.";

Proc. Natl. Acad. Sci. U.S.A. 84:5625-5629(1987).

PROTEIN LOCATION: DIEDER PROTEIN LACKS BOTH NEURAMINIDASE AND HEMAGGLUTINATING ACTIVITIES.

PROTEILULAR LOCATION: EXPRESSED ON THE SURFACE OF THE INFECTED CELLS AND INCORPORATED IN THE MEMBRANE OF THE VIRIONS.

PROTEIL BAY CARRY 40-80 SEBARATE O-LINKED CARBONYDRATE CHAINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human respiratory syncytial virus (subgroup A / strain Long). Viruses; ssRNA negative-strand viruses; Mononegavirales; Paramyxoviridae; Pneumovirinae; Pneumovirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Johnson P.R., Spriggs M.K., Olmsted R.A., Collins P.L.; "The G glycoprotein of human respiratory syncytial viruses subgroups A and B: extensive sequence divergence between
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Major
                                                                                                                                                                                                                                                                            PIR; A32703; MGNZRI
                                                                                                                                                                                                                                                                                         EMBL; M17212;
                                                                                                                                                                                                                                                                                                                or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                          modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                      use
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between the Swiss Institute of Bioinformatics and the EMBL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Paramyxoviridae;
NCBI_TaxID=11260;
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ce glycoprotein G (Attachment
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N-LINKED (GLCNAC...) (POI
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01-AUG-1992 (Rel. 23, Created)
01-AUG-1992 (Rel. 23, Last sequence update)
01-AUG-1992 (Rel. 23, Last annotation update)
Major surface glycoprotein G (Attachment glyco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             P27026;
01-AUG-1992
01-AUG-1992
01-AUG-1992
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SEQUENCE
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CARBOHYD
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J. Gen. Virol. 72:2091-2096(1991).

-:- FUNCTION: UNLIKE THE OTHER PARAMYXOVIRUS ATTACHMENT PROTEINS, TRESPIRATORY SYNCYTIAL VIRUS G PROTEIN LACKS BOTH NEURAMINIDASE HEMAGGLUTINATING ACTIVITIES.

-:- SUBCELLULAR LOCATION: EXPRESSED ON THE SURFACE OF THE INFECTED CELLS AND INCORPORATED IN THE MEMBRANE OF THE VIRIONS.

-:- PTM: MAY CARRY 40-80 SEPARATE O-LINKED CARBOHYDRATE CHAINS DISTRIBUTED AMONG THE 91 SERINE AND THREONINE RESIDUES.
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Cane P.A., Matthews D.A., Pringle C.R.; "Identification of variable domains of the subgroup A respiratory syncytial viruses.";
                                                                                                                                                                                                                                      Viruses; ssRNA negative-strand viruses; Paramyxoviridae; Pneumovirinae; Pneumovir
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Paramyxoviridae; Pneumovirinae;
                                                                                                                       SEQUENCE FROM N.A. MEDLINE-91374005; Pubmed-1895054;
                                                                                                                                                                                                                                                                                                                                                                  Human respiratory syncytial virus (strain rsb6614)
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"Identification of variable domains of the attachment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WEDLINE=91374005; PubMed=1895054;
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es; ssRNA negative-strand viruses; Mononegavirales;
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-!- FUNCTION: UNLIKE THE OTHER PARAMYXOVIRUS ATTACHMENT PROTEINS, T
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                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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-!- PTM: MAY CARRY 40-80 SEPARATE O-LINKED CARBOHYDRATE CHAINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human respiratory syncytial virus (subgroup B / strain 18537).
Viruses; ssRNA negative-strand viruses; Mononegavirales;
Paramyxoviridae; Pneumovirinae; Pneumovirus.
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(Rel. 17, Last sequence update)
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ce glycoprotein G (Attachment glyco
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Pred. No. 6
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EMBL; M17213; AAA47412.1; PIR; B32703; MGNZ18.

InterPro;

IPR000925; Glycoprot\_G.
0802; Glycoprotein\_G: 1.

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VGLG_HRSV8
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EMBL: M5500-.

EMBL: M73545; AAA4/400.

( PIR: A37077; MGNZ60.

R Interpro; IPR000925; Glycoprotein_G: 1.

R Pfam: PF00802; Glycoprotein_G: 1.

KW Transmembrane: Glycoprotein.

FT DOMAIN

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Matches 21; Conser
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P23041;
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CARBOHYD
CARBOHYD
CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                            Sullender W.M., Mufson M.M., Anderson "Genetic diversity of the attachment respiratory syncytial viruses.";
J. Virol. 65:5425-5434(1991).
                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sullender W.M., Anderson K., Wertz G.W.;
The respiratory syncytial virus subgroup B attachment glycoprotein:
analysis of sequence, expression from a recombinant vector, and
evaluation as an immunogen against homologous and heterologous
subgroup virus challenge.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-NOV-1991
01-AUG-:1992
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Major
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human respiratory syncytial virus (subgroup B / strain 8/60).
Viruses; ssRNA negative-strand viruses; Mononegavirales;
Paramyxoviridae; Pneumovirinae; Pneumovirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=90357765; PubMed=1697126;
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                                                                                                                                                                    or send
                                                                                                                                                                                    entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=91374595; PubMed=1895391;
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PTM: MAY CARRY 40-80 SEPARATE O'LINKED CARBOHYDRATE CHAINS DISTRIBUTED AMONG THE 91 SERINE AND THREONINE RESIDUES.
                                                                                                                                                                                                                                                                                                                                                   FUNCTION: UNLIKE THE OTHER PARAMYXOVIRUS ATTACHMENT PROTEINS, 7 RESPIRATORY SYNCYTIAL VIRUS G. PROTEIN LACKS BOTH NEURAMINIDASE HEMAGGLUTINATING ACTIVITIES.
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(Rel. 20, Last sequence update)
(Rel. 23, Last annotation update)
ce glycoprotein G (Attachment glycoprotein
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BC8C59F69CA7AFC2 CRC64;
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SEQUENCE
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                                                                                                                            DISULFID DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mallipeddi S.K., Samal S.K.;

"Analysis of the ovine respiratory syncytial virus (RSV) G glycoprotein gene defines a subgroup of ungulate RSV.";

J. Gen. Virol. 74:2787-2791(1993).

-!- FUNCTION: UNLIKE THE OTHER PARAMYXOVIRUS ATTACHMENT PROTEINS, RESPIRATORY SYNCYTIAL VIRUS G PROTEIN LACKS BOTH NEURAMINIDAS!
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CARBOHYD
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Transmembrane; Glycoprotein.
DOMAIN 1 37 C.
                                                                                                                                                                                                                                                                                                                EMBL; S67863; AAB29551.1;
EMBL; S67862; AAB29551.1;
HSSP; P22261; 1BRV
                                                                                                                                                                                                                                                                                                                                                                                                        modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Entropean Bioinformatics Institute. There are no restiuse by non-profit institutions as long as its content
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -!- SUBCELLULAR LOCATION: EXPRESSED ON THE SURFACE OF THE INFECT CELLS AND INCORPORATED IN THE MEMBRANE OF THE VIRIONS.
-!- SIMILARITY: TO THE G PROTEINS OF EITHER THE SUBGROUP A OR B
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16-OCT-2001
                                            GD_DROME

O62589;

16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
16-OCT-2001 (Rel. 40, Cast annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Diaminopimelate epimerase DAPF OR PM1703.
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modified and this statement is not removed.
entities requires a license agreement (See l
or send an email to license@isb-sib.ch).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Pterygota; Neoptera; Endopterygota; Diptera; Brachyc Ephydroidea; Drosophilidae; Drosophila.
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ACT_SITE 217 217 BY SIMILARITY
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Pfam; PF01678; DAP_epimerase; 1.
PROSITE: PS01326; DAP_EPIMERASE; 1.
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16-OCT-2001
                       Drosophila melanogaster (Fruit fly)
Eukaryota; Metazoa; Arthropoda; Tra
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8; Conserv
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t annotation update)
(EC 5.1.1.7) (DAP epimerase).
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RA Ballew R.M., Basu A., Basndale J., Bayraktaroglu L., Beasley E.M.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Botlshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Botlshakov S.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Daves P.,
RA Ge Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Clodek M.J., Evangelista C.C., Ferraz C., Ferritera S., Fleischman M.,
RA Clodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M..
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lei Z.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lei Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lei Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Kelson D.R., Nelson K.A., Nixon K., Nussers D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Shue S., Wassarman D.A., Weinstock G.M., Weissenbach J.,
RA Weisson D.R., Nelson K.A., Nixon K., Wenter E., Wang A., H., Wang Y., Yen Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
RA Weins S.M., Woodage T. Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Weinson S.M., Moodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Weinson S.M., Moodage T. Worley K.C., Wu D., Yang S., Zhao Q., Zheng L.,
RA Yeng Y.H., Zhong F.N., Rubin G.M., Venter E., Wang A., H.,
RA Sheng X.H., Zhong F.N., Rubin G.M., Venter E., Wang A., Sheng L.,
RA Yeng Y.H., Zhong F.N., Rubin G.M., Venter E., Wang X., Saith H.O.,
RA Yelly S.M., Weinstock G.M., Weissenbach J.,
RA Weinson S.M., Woodage T. Worley K.C., Wu D., Yang S., Zhao Q., Zheng T.,
RA Yelly S.M., Weinstock G.M., Weissenbach J.,
RA Yelly S.M., Weinstock G.M., Weinstock 
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Baldwin D.,
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RESULT 14
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Pfam; PF00089; trypsin; 1.

PRINTS; PR00722; CHYMOTRYPSIN.

SMARR; SM0020; Tryp_SPC; 1.

SMARR; SM0020; TRYPSIN_Dow; 1.

PROSITE; PS00240; TRYPSIN_HIS; FALSE_NEG.

PROSITE; PS00135; TRYPSIN_SER; FALSE_NEG.

PROSITE; PS00135; TRYPSIN_SER; Glycoprotein;
                                            "Genome sequence of the endocellular bacterial symbiont of aphids Buchnera sp. APS.";
Nature 407:81-86(2000).

"IF FUNCTION: THIS PROTEIN SPECIFICALLY CATALYZES THE REMOVAL OF SIGNAL PEPTIDES FROM PROLIPOPROTEINS (BY SIMILARITY).

"I- CATALYTIC ACTIVITY: Cleavage of N-terminal leader sequences from membrane prolipoproteins. Hydrolyses Xaa-Xbb-xbb-|-Cys, in which Xaa is hydrophobic (preferably Leu), Xbb is often Ser or Ala, Xcc is often Gly or Ala, and the Cys is alkylated on sulfur with a diacylglyceryl group.

"I- SUBCELLULAR LOCATION: Integral membrane protein (Probable)."
                                                                                                                                                                                                                                                                                                                   LSPA_BUCAI STANDARD: PRT: 160 AA. P57248;
16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Li-OCT-2001 (Rel. 40, Last annotation update)
Li-Opprotein signal peptidase (EC 3.4.23.36) (Prolipoprotein peptidase) (Signal peptidase II) (SPase II).
LSPA OR BU148
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STRAIN-TOKYO 1998;
MEDLINE-20445173; PubMed-10993077;
Shigenobu S., Watanabe H., Hattori
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                   Bacteria;
                                                                                                                                                                                                                                                                                             symbiotic bacterium)
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InterPro; IPR001254; Trypsin.
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SEQUENCE FROM N.A.
STRAIN=K12 / MG1655;
STRAIN=92358234; PubMed=1379743;
MEDLINE=92358234; PubMedE=1379743;
Daniels D.L., Plunkett G. III, Burland V.D., E
"Analysis of the Escherichia coli genome: DNA
from 84.5 to 86.5 minutes.";
Science 257:771-778(1992).
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PO8885; P78126;

01-NOV-1988 (Rel. 09, Creat

30-MAY-2000 (Rel. 39, Last

16-OCT-2001 (Rel. 40, Last
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InterPro; IPR001872; Lipo_sig_PTase.
Pfam; PF01252; Peptidase_A8; 1.
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"The
                                                                                                                                                                                                                                                          STRAIN=K12 / MG1655;
MEDLINE=97426617; PubMed-9278503;
Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burl Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew
                                                                                                                                                                                                        Gregor J., Da
Mau B., Shao
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN-K12
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                           STRAIN=K12;
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CONFLICT 98 98 T -> S (IN REF. 3).

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J. Bacteriol. 172:6973-6980(1990).
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Biochimie 78:277-287(1996).
-i- CATALYTIC ACTIVITY: LL-2,6-diaminoheptanedioate - meso-
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-!- PATHWAY: SIXTH STEP IN THE BIOSYNTHESIS OF LYSINE FROM ASPARTATE
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    -1- SUBCELLULAR LOCATION: Cytoplasmic.
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Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                     Sullender W.M., Mufson M.A., Prince G., Anderson L.J., Wertz G.W.;
"Antigenic and genetic diversity among the attachment proteins of
group A respiratory Syncytial viruses that have caused repeat
infections in children.";
J. Infect. Dis. 178.925-922(1998).
EMBL; AF065408; AAD02944.1;
InterPro; IPR000925; Glycoprot_G.
InterPro; IPR009925; Glycoprot_G.
InterPro; IPR003880; Phosphopant_attach.
InterPro; IPR003880; Phosphopant_attach.
Pfam; PF00802; Glycoprotein_G;
PFINTS; PR01217; PRICHEXTENSN.
PRSNITE; PR01217; PRICHEXTENSN.
PROSITE; PS00012; PHOSPHOPANTETHEINE; UNKNOWN_1.
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                                                                                                                                                                                                                                                                                                                                                          NON_TER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN=WV19983; MEDLINE-99022964; PubMed=9806017;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human respiratory syncytial virus.
Viruses; ssRNA negative-strand viruses; Mononegavirales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
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NCBI_TaxID=11250;
144 KQRQNKPPSKPNNDFHFEVFNFVPCSIC 171
                                             1 KQRQNKPPSKPNNDFHFEVFNFVPCSIC 28
                                                                                                                                                              28;
                                                                                                                                                          Similarity 100 28; Conservative
                                                                                                                                                                                                                                                                                                                                                          292 AA;
                                                                                                                                                                                                                                                                                                                                                          31964 MW;
                                                                                                                                                                                           96.48;
                                                                                                                                                          0;
                                                                                                                                                                                                    Score 163;
Pred. No.
                                                                                                                                                          Mismatches
                                                                                                                                                                                                                                                                                                                                                          8942A8DD0A402A4B CRC64;
                                                                                                                                                                                                                                     DB 12;
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Best Local S
Matches 28
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Q86356;
01-NOV-1996 (TrEMBLrel. (
01-NOV-1996 (TrEMBLrel. (
01-DEC-2001 (TrEMBLrel. 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ol-MAY-1999 (TrEMBLrel. 10, Created)
Ol-MAY-1999 (TrEMBLrel. 10, Last sequence update)
Ol-JUN-2001 (TrEMBLrel. 17, Last annotation update)
ATTACHMENT GLYCOPROTEIN G (FRAGMENT).
Human respiratory syncytial virus.
Viruses; ssRNA negative-strand viruses; Mononegavirales;
Paramyxoviridae; Pneumovirinae; Pneumovirus.
NCBI_TaxID-11250;
Cane P.A.;

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J. Infect. Dis. 178:925-932(1998).
EMBL; AF065407; AAD02943.1;
InterPro; IPR000925; Glycoprot_G.
InterPro; IPR003880; Phosphopant_attach.
InterPro; IPR002965; P_rich_extensn.
                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
STRAIN-RSB89-1734:
MEDIANE-913174005; PubMed-1895054;
Cane P.A., Matthews D.A., Pringle C.R.;
"Identification of variable domains of the subgroup A resphatory syncytial vuruses.";
J. Gen. Virol. 72:2091-2096(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 respiratory syncytial virus.
Viruses; ssRNA negative-strand viruses; Mononegavirales;
Paramyxoviridae; Pneumovirinae; Pneumovirus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN=WV6973;
MEDLINE=99022964; PubMed=9806017;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Paramyxoviridae;
NCBI_TaxID=12814;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 G PROTEIN (FRAGMENT). respiratory syncytial
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PRINTS: PR01217: PRICHEXTENSN.
PROSITE: PS00012: PHOSPHOPANTETHEINE: UNKNOWN_1.
                                                                                                                                                                                                                 SEQUENCE FROM N.A. STRAIN-RSB89-1734;
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Similarity 100.0%;
28; Conservative (
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Pred. No.
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Best Local S
Matches 28
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Q82066;
01-NOV-1996 (TrEMBLrel. C
01-NOV-1996 (TrEMBLrel. C
01-DEC-2001 (TrEMBLrel. 1
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Q86360;
01-NOV-1996 (TIEMBLIEL 0
01-NOV-1996 (TIEMBLIEL 0
01-DEC-2001 (TIEMBLIEL 1
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SEQUENCE
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NON_TER
SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (APR-1993) to the EMBL/GenBank/DDBJ EMBL; X73354; CAA51765.1; -
InterPro; IPR000925; Glycoprot_G.
InterPro; IPR003880; Phosphopant_attach.
Pfam; PF00802; Glycoprotein_G; 1.
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MEDLINE=91374005; PubMed=1895054;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    respiratory syncytial virus.
Viruses; ssRNA negative-strand '
Paramyxoviridae; Pneumovirinae;
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SEQUENCE FROM N.A. STRAIN=SUBGROUP A; MEDLINE=94335057;
                                                                                                                     Paramyxoviridae;
NCBI_TaxID=11250;
                                                                                                                                                                                  Viruses;
                                                                                                                                                                                      Human respiratory syncytial virus.
Viruses: ssRNA negative-strand viruses:
                                                                                                                                                                                                                                                                                    GLYCOPROTEIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN-RSB89-642;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Paramyxoviridae;
NCBI_TaxID=12814;
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Pred. No.
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Last annotation updat
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01-NOV-1996
01-DEC-2001
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J. Virol. 68.5448-5459(1994).
EMBL; 233428; CANB3871.1;
InterPro; IPR000925; Glycoprot_G.
InterPro; IPR003880; Phosphopant_attach.
Pfam; PF00802; Glycoprotein_G; J.
PROSITE; PS00012; PHOSPHOPANTETHEINE; UNKNOWN_1.
SEQUENCE 297 AA; 32555 MW; 9D0A69BECAE8B6C8 CRC64;
                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
STRAIN-SUBGROUP
MEDLINE-94335057; PubMed-8057427;
Garcia O., Martin M., Dopazo J., Arbiza
Hortal M., Perez-Brena P., Martinez I.,
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InterPro; IPR003880; Phossphopant_attach.
Pfam; PF00802; Glycoprotein_G; J.
PROSITE; PS00012; PHOSPHOPANTETHEINE; UNKNOWN_1.
SEQUENCE 297 AA; 32589 MW; F210F8C68193F5DD CRC64;
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J. Virol. 68.5448-5459(1994).
EMBL: 233427: CAA83870.1;
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Viruses; ssRNA negative-strand viruses; Mononegavirales;
Paramyxoviridae; Pneumovirinae; Pneumovirus.
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01-NOV-1996 (TrEMBLrel. 01,
01-NOV-1996 (TrEMBLrel. 01,
01-DEC-2001 (TrEMBLrel. 19,
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SEQUENCE FROM N.A.
STRAIN-SUBGROUP A;
MEDLINE-94335057; PubMed-8057427;
MEDLINE-9435057; PubMed-8057427;
MEDLINE-945757; PubMed-8057427;
MEDLINE-945757; PubMed-8057427;
MEDLINE-945757; PubMed-8057427;
MEDLINE-945757; PubMed-8057427;
MEDLINE-95757; PubMed-805767;
MEDLINE-95757; PubMed-805767;
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01-MAY-1999
01-MAY-1999
01-JUN-2001
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Viruses; ssRNA negative-strand viruses; Mononegavirales;
Paramyxoviridae; Pneumovirinae; Pneumovirus.
NCBI_TaxID-11250;
                                                                                                                                                                                          J. Infect. Dis. 178:925-932(1998).

EMBL, AF065405; AAD02941.1; -.
InterPro; IPR000925; Glycoprot.G.
InterPro; IPR003880; Phosphopant_attach.
InterPro; IPR002965; P_rich_extensn.
Pfam; PF00802; Glycoprotein_G; 1.
PFINTS; PR001217; PRICHEXTENSN.
PROSITE: PS000121; PHOSPHODANTETHEINE; UNKNOWN_1.
SEQUENCE 297 AA; 32572 MW; 5C10E719A05EF5C1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLIN-99022964; Pubmed-9806017;
MEDLIN-99022964; Pubmed-9806017;
MEDLIN-99022964; Pubmed-9806017;
MEDLIN-99022964; Pubmed-9806017;
MEDLIN-99022964; Pubmed-9806017;
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InterPro; IPR003880; Phosphopant_attach.
Pfam; PF00802; Glycoprotein_G; IPR003802; Glycoprotein_G; IPR00387E; PS00012; PHOSPHOPANTETHEINE; UNKNOWN_1.
SEQUENCE 297 AA; 32581 MW; AD947B2318193306 CRC64;
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EMBL: 233432: CAA83875.1;
                                                                                                                                                                                                                                                                                                                                                                                              "Antigenic and genetic diversity among group A respiratory syncytial viruses infections in children.";
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NCBI_TaxID=11250;
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Viruses; ssRNA negative-strand viruses; Mononegavirales;
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Garcia-Barreno B.,
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J. Infect. Dis. 181:1547-1556(2000).

J. Infect. Dis. 181:1547-1556(2000).

EMBL; AF193305; AAF23728.1;

InterPro; IPR000925; Glycoprot_G.

InterPro; IPR00380; Phosphopant_attach.

InterPro; IPR00380; Phosphopant_attach.

InterPro; IPR002965; Prich_extensn.

Pfam; PF00802; Glycoprotein_G; 1.

PRINTS; PR01217; PRICHEXTENSN.

PROSITE; PS00012; PHOSPHOPANTETHEINE; UNKN.

NON_TER

SEQUENCE 278 AA; 30461 MW; AC113DCCDCF
                                                             "Genetic diversity and molecular epidemiology of the subgroups A and B of respiratory syncytial virus is consecutive epidemics in Korea.";

J. Infect. Dis. 181:1547-1556(2000).

EMBL; AF193309; AAF23732.1;

InterPro; IPR003925; Glycoprot_G.

InterPro; IPR003925; Glycoprot_G.

InterPro; IPR00380; Phosphopant_attach.
InterPro; IPR003965; P_rich_extensn.

Pfam; PF00802; Glycoprotein_G; 1.

PRINTS; PR01217; PRICHEXTENSN.

PROSITE: PS00012; PHOSPHOPANTETHEINE; UNKNOWN_1.
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Q9Q6U1;
Q1-MAY-2000
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Q9Q6T7;
Q1-MAY-2000 (TrEMBLrel.
PRINTS; P
PROSITE;
NON_TER
SEQUENCE
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01-DEC-2001
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Choi E.H., Lee H.J.;
"Genetic diversity and molecular epidemiology of
subgroups A and B of respiratory syncytial virus
consecutive epidemics in Korea.";
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01-MAY-2000 (TrEMBLrel.
01-DEC-2001 (TrEMBLrel.
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Viruses; ssRNA negative-strand viruses; Mononegavirales;
Paramyxoviridae; Pneumovirinae; Pneumovirus.
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Viruses; ssRNA negative-strand viruses; Mononegavirales;
Paramyxoviridae; Pneumovirinae; Pneumovirus.
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       B33F085F89E1A9D0 CRC64;
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0906T3;

01-MAY-2000 (TrEMBLrel. 13,

01-MAY-2000 (TrEMBLrel. 13,

01-DEC-2001 (TrEMBLrel. 19,
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J. Infect. Dis. 181:1547-1556(2000).
EMBL; AF193312; AAF23755.1; -.
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Q9Q6T4;
Q1-MAY-2000 (TrEMBLrel. 13,
Q1-MAY-2000 (TrEMBLrel. 13,
Q1-DEC-2001 (TrEMBLrel. 19,
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NCBI_TaxID=11250;
MEDLINE=20283719; PubMed=10823752;
Choi E.H., Lee H.J.;
"Genetic diversity and molecular e
subgroups A and B of respiratory s
                                                                                                                                                                            Human respiratory syncytial virus.
Viruses; ssRNA negative-strand viruses; Mononegavirales;
Paramyxoviridae; Pneumovirinae; Pneumovirus.
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InterPro; IPR003880; phosphopant_attach
InterPro; IPR002965; p_rich_extensn.
Pfam; PF00802; Glycoprotein_G; 1.
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Viruses; ssRNA negative-strand viruses; Mononegavirales;
Paramyxoviridae; Pneumovirinae; Pneumovirus.
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| Similarity 96.4%;
| 27; Conservative
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Matches 27; Conserv
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J. Infect. Dis. 181:1547-155(2000).

EMBL: AF19313: AAF23736.1;
InterPro: IPR000925; Glycoprot_G.
InterPro: IPR003880; Phosphopant_attach.
InterPro: IPR002965; P_1ich_extensn.
Pfam; PF00802; Glycoprotein_G: 1
PRINTS; PR01217; PRICHEXTENSN.
PROSITE; PS00012; PHOSPHOPANTETHEINE; UNKNOWN_1.
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01-MAY-2000
01-DEC-2001
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"Genetic diversity and molecular epidemiology of the G protein of genetic diversity and molecular epidemiology of the G protein on the Groups of the G protein of the Groups of the G protein of the Groups 
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Viruses; ssRNA negative-strand viruses; Mononegavirales;
Paramyxoviridae; Pneumovirinae; Pneumovirus.
NCBI_TaxID-11250;
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01-MAY-2000 (TrEMBLrel. 13,
01-DEC-2001 (TrEMBLrel. 19,
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nilarity 96.4%;
Conservative
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: Pred. No. 2.!
1; Mismatches
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01-MAY-2000
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"Genetic diversity and molecular epidemiology of the G protein subgroups A and B of respiratory syncytial virus isolated over consecutive epidemics in Korea.";

J. Infect. Dis. 181:1547-1556(2000).

EMBL; AF193306; AAF23729.1;
InterPro; IPR000925; Glycoprot_G.

InterPro; IPR003880; Phosphopant_attach.
                                                                                                                                                                                                                                                                                                                                 "Genetic diversity and molecular epidemiology of the G protein of subgroups A and B of respiratory syncytial virus isolated over 9 consecutive epidemics in Korea.";
J. Infect. Dis. 181:1547-1556(2000).
EMBL: AF193307; AAF23730.1;
InterPro; IPR003880; Phosphopant_attach.
InterPro; IPR003880; Phosphopant_attach.
InterPro; IPR00385; P_rich_extensn.
                                                                                                                                                                                                              Pfam; PF00802; Glycoprotein_G; 1.....
PRINTS; PR01217; PRICHEXTENSN.
PROSITE; PS00012; PHOSPHOPANTETHEINE; UNKNOWN_1.
NON_TER 1 1
SEQUENCE 279 AA; 30570 MW; AE6CF9C1D8F8A97C
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Viruses; ssRNA negative-strand viruses; Mononegavirales;
Paramyxoviridae; Pneumovirinae; Pneumovirus.
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NCBI_TaxID=11250;
[1]
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Viruses; ssRNA negative-strand viruses; Mononegavirales;
Paramyxoviridae; Pneumovirinae; Pneumovirus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN-91399;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=20283719; PubMed=10823752;
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                                             1 KQRQNKPPSKPNNDFHFEVFNFVPCSIC
KQRQNKPPNKPNNDFHFEVFNFVPCSIC
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27; Conservative
                                                                                              27; Conser
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Pred. No. 2
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Search completed: September 4, 2002, 17:37:34 Job time: 123 sec

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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Sequence:
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Maximum DB seq length: 200000000
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101
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BLOSUM62
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169
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/cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
/cgn2_6/ptodata/2/iaa/6A_COMB.pep:*
/cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
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DВ
          US-08-467-963C-8
US-08-838-139D-8
US-08-8467-961A-8
US-08-8467-961A-8
US-08-144-639E-8
US-08-144-639E-8
US-08-793-792-13
US-08-793-792-11
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US-08-793-792-13
US-08-846-68-8
US-08-793-792-6
US-08-793-792-6
US-08-793-792-6
US-08-793-792-6
US-08-793-792-10
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(without alignments)
54.446 Million cell updates/sec
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NUMBER OF SEQUENCES: 19
CURRENT APPLICATION UNBER: US/07/543,780
FILING DATE: 31-OCT-1988
PRIOR APPLICATION DATA:
APPLICATION UNBER: 137,387
FILING DATE: 23-DEC-1987
SEQ ID NO:19: 661

5194595-19

LENGTH: 681

28 45.5 26.9 52 4 US-09-346-510B-22 Se 29 45.5 26.9 154 4 US-08-871-732A-1 30 45.5 26.9 154 4 US-08-871-732A-1 31 45.5 26.9 727 2 US-08-475-804-9 32 45.5 26.9 727 2 US-08-475-804-9 32 45.5 26.9 728 5 PCT-US95-08429-9 33 45.5 26.9 728 5 PCT-US95-08429-9 34 45.5 26.9 728 5 PCT-US95-08429-9 35 44.5 26.6 30.9 3 US-08-605-284B-4 36 44.5 26.3 14.9 3 US-08-8134-57D-2 39 44.5 26.3 477 4 US-09-128-142-4 40 44.5 26.3 477 4 US-09-128-142-4 41 44 26.0 30.9 3 US-08-605-284B-6 42 44 26.0 30.9 3 US-08-605-284B-10 43 44 26.0 310 3 US-08-605-284B-14 44 26.0 310 3 US-08-605-284B-14 45 46 26.0 310 3 US-08-605-284B-14 46 26.0 310 3 US-08-605-284B-14 47 48 26.0 310 3 US-08-605-284B-14 48 26.0 310 3 US-08-605-284B-14 49 40 26.0 310 3 US-08-605-284B-14 40 41 26.0 310 3 US-08-605-284B-14 41 42 26.0 310 3 US-08-605-284B-14 42 43 26.0 310 3 US-08-605-284B-14 43 44 26.0 310 3 US-08-605-284B-14 44 26.0 310 3 US-08-605-284B-14 45 44 26.0 310 3 US-08-605-284B-14 46 26.0 310 3 US-08-605-284B-15 47 48 26.0 310 3 US-08-605-284B-15 48 49 26.0 310 3 US-08-605-284B-14 49 40 26.0 310 3 US-08-605-284B-15 49 40 40 26.0 310 3 US-08-605-284B-14 40 41 26.0 310 3 US-08-605-284B-14 41 42 26.0 310 3 US-08-605-284B-14 42 43 26.0 310 3 US-08-605-284B-14 43 44 26.0 310 3 US-08-605-284B-14 44 26.0 310 3 US-08-605-284B-14 45 46 26.0 310 3 US-08-605-284B-14 46 26.0 310 3 US-08-605-284B-14 47 48 26.0 310 3 US-08-605-284B-14 48 26.0 310 3 US-08-605-284B-14 49 26.0 310 3 US-08-605-284B-14 49 26.0 310 3 US-08-605-284B-14 40 40 26.0 310 3 US-08-605-284B-14 40 40 26.0 310 3 US-08-605-284B-14 41 42 43 26.0 310 3 US-08-605-284B-14 42 43 26.0 310 3 US-08-605-284B-14 43 44 26.0 310 3 US-08-605-284B-14 44 26.0 310 3 US-08-605-284B-15 48 49 49 49 49 49 49 49 49 49 49 49 49 49	RESULT 1 5194595-19 ;Patent NO. 5194 ; PATENT: TITLE OF IN ;IMMUNOGENIC SEG		45	44	43	42	41	40	39	38	37	36	35	34	33	32	31	30	29	28
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RESULT 2
US-08-467-963C-8
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Best Local
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                                                                                                                                                                                                           GENERAL INFORMATION:

APPLICANT: KLEIN, Michel H

APPLICANT: DI, Run-Pan

APPLICANT: DI, Run-Pan

APPLICANT: DE RASYSHYN, MARY E

TITLE OF INVENTION: MULTIMERIC HYBRID GENE ENCODING A

TITLE OF INVENTION: PARAINFLUENZA VIRUS AND RESPIRATORY SYNCYTIAL VIRUS

TITLE OF INVENTION: PARAINFLUENZA VIRUS AND RESPIRATORY SYNCYTIAL VIRUS
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                       NUMBER OF SEQUENCES: 3
                                                         STREET: 6th Floc
CITY: Toronto
STATE: Ontario
COUNTRY: Canada
ZIP: M5G 1R7
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                                                                                                                                                         ADDRESSEE:
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28; Conserv
                                                                                                                                   6th Floor, 330 University Avenue
                                                                           Canada
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                                                                                                                                                         Sim & McBurney
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100.0%; Pred. No. 2
tive 0; Mismatches
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COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/838,189D
FILING DATE: 16-APR-1997
CLASSIFICATION: 435
PRIOR APPLICATION NUMBER: US 08/001,554
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TELEFAX: (416) 595-1163
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE: 06-JAN-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9200117.1
FILING DATE: 06-JAN-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: MULTIMERIC HYBRID GENE ENCODING A TITLE OF INVENTION: CHIMERIC PROTEIN WHICH CONFERS PROTECTION AGAINST TITLE OF INVENTION: PARAINFLUENZA VIRUS AND RESPIRATORY SYNCYTIAL VIRUS NUMBER OF SEQUENCES: 38
FILIAN FOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: GB 9200117.1
FILING DATE: 06-JAN-1992
                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
ADDRESSEE: Sim & McBurney
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TELECOMMUNICATION INFORMATION:
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OTTY: Toronto

Ontario
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TYPE: a
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REGISTRATION NUMBER: 24,973
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US 0 FILING DATE: 16-APR-1997
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                                                                                                                                                                                                                                                                               COUNTRY:
                                                                                                                                                                                                                                                                                                   STATE: Ontario
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amino acid
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In Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                     330 University Avenue
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Pred. No. 2.5e-15;
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US-08-838-189D-8
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Best Local
                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/344,639
FILING DATE: 14-NOV-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9200117.1
FILING DATE: 06-JAN-1992
ATTORNEY/AGENT INFORMATION:
NAME: STEWART, Michael:
NAME:
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INFORMATION FOR SEQ ID NO:
                         TELEPHONE: (416) 595-1155
TELEFAX: (416) 595-1163
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
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APPLICANT:
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LENGTH: 298 amino acid
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MEDIUM TYPE: Floppy disk
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                                                                                                                                                                    REFERENCE/DOCKET NUMBER: 10 TELECOMMUNICATION INFORMATION:
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TITLE OF INVENTION:
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TYPE: amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US/O
FILING DATE: 07-MAY-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRANDEDNESS:
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                                                                                                                                                                                                                                              REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CITY: Toronto
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27; Conserv
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M5G 1R7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                6th Floor,
298 amino acids
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EWASYSHYN, MATY E
EWASYSHYN, MATY E
VENTION: CHIMERIC PROTEIN WHICH CONFERS PROTECTION
VENTION: AGAINST PARAINFLUENZA VIRUS AND RESPIRATORY
VENTION: SYNCYTIAL VIRUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
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Pred. No. 2.5e
1; Mismatches
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Best Local Similarity
Matches 27; Conser
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9200117.1
FILING DATE: 06-JAN-1992
                                                                                                                                                                                                                                                                                            REFERENCE/DOCKET NUMBER: 10
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: Patentin Rei
CURRENT APPLICATION DATA
                                                                                                                                            TOPOLOGY: linear MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
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TITLE OF INVENTION:
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OPERATING SYSTEM:
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                                                                                                                                                                         STRANDEDNESS:
                                                                                                                                                                                       TYPE: amino acids
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TELEX: 065-24567 SIMBAS
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                                                                                                                                                                                                                                                                                                                          NAME: Stewart, Michael REGISTRATION NUMBER: 2
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                1 KQRQNKPPSKPNNDFHFEVFNFVPCSIC 28
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                                                         Conservative
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CHIMERIC PROTEIN WHICH CONFERS
PROTECTION AGAINST PARAINFLUENZA VIRUS
AND RESPIRATORY SYNCYTIAL VIRUS
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                                                                       94.7%;
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                                                                                                                                                                                                                                                                                                           1038-391 MIS
                                                  Pred. No. 2.5e
1; Mismatches
                                                                       Score 160; DB 3; Pred. No. 2.5e-15;
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2.5e-15;
                                                                                   Length 298;
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US-08-467-961A-8
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Best Local Similarity
Matches 27; Conserv
                                                                                                          Sequence 8, Application US/08467961A Patent No. 6171783
                                                                          GENERAL INFORMATION:
APPLICANT: Klein,
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SEQUENCE CHARACTERISTICS:
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APPLICANT:
                            APPLICANT: Du, Run-Pa
APPLICANT: Ewasyshyn,
TITLE OF INVENTION: C
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REFERENCE/DOCKET NUMBER: 10
TELECOMMUNICATION INFORMATION:
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ZIP: M5G 1R7
COMPUTER READABLE FORM:
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APPLICATION NUMBER:
FILING DATE: 06-JAN-
CLASSIFICATION: 435
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NAME: Stewart, Michael I
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              APPLICANT: Du, Run-Pan
APPLICANT: Ewasyshyn, Mary E
TITLE OF INVENTION: Chimeric
NUMBER OF SEQUENCES: 21
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CORRESPONDENCE ADDRESS:
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OPERATING SYSTEM:
SOFTWARE: Patent!
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STATE:
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065-24567 SIMBAS
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                                                                            Klein, Michel H
                                                                                                                                                                                                                                                                      Conservative
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SYSTEM: PC-DOS/MS-DOS
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Pred. No. 2.5e-15;
                             Immunogens
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REGISTRATION NUMBER: 24,973
REFERENCE/DOCKET NUMBER: 1038
TELECOMMUNICATION INFORMATION:
TELEPHONE: (416) 595-1155
TELEFAX: (416) 595-1163
TELEFAX: (416) 595-1163
TELEFAX: 065-24567 SIMBAS
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 298 amino acids
                                                                                                                                           APPLICANT: Du, Run-rau
APPLICANT: Ewasyshyn, Mary E
TITLE OF INVENTION: Chimeric Immunogens
NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sim & McBurney
STREET: 330 University Avenue, 6th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
Matches 27; Conserv
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APPLICATION NUMBER: US 08/001,554
FILING DATE: 06-JAN-1993
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/
FILING DATE: 06-JUN-199
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MEDIUM TYPE: Floppy disk
             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0
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ATTORNEY/AGENT INFORMATION:
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PRIOR APPLICATION DATA:
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                                                                                                                                     STREET: 330 Uni
CITY: Toronto
STATE: Ontario
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OPERATING SYSTEM: PC-DOS/MS-DOS
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ZIP: M5G 1R7
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TOPOLOGY: lir
                                                                                                         COUNTRY: Canada
ZIP: M5G 1R7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 KORONKPPSKPNNDFHFEVFNFVPCSIC 28
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ARE: Patentin Release #1.0, Version #1.25 APPLICATION DATA:
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330 University Avenue, 6TH Floor
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Pred. No. 2
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Best Local Similarity
Matches 27; Conserv
                                                                                                                                                                                    COUNTRY: COADAGA

ZIP: M5G 1R7

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

COMPUTER: IBM PC compatible

COMPUTER: PATENT: PC-DOS/MS-DOS

SOFTWARE: PATENTIN Release #1.0, v

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/750,624

FILING DATE: 26-FEB-1997

CLASSIFICATION: 424

ATTORNEY/AGENT INFORMATION:

NAME: Stewart, Michael I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 9,
                                                                                   TELEFAX: (416) 595-1163 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     tent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: James, Olive A APPLICANT: Chong, Pele APPLICANT: Klein "ITTLE"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELECOMMUNICATION INFORMATION: TELEPHONE: (416) 595-1155
                                                                                                                    REFERENCE/DOCKET NUMBER: 10
TELECOMMUNICATION INFORMATION:
TELEPHONE: (416) 595-1155
                                                                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
ADDRESSEE: Sim & McBurney
STREET: 6th Floor, 330 University Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: 1
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ATTORNEY/AGENT INFORMATION:
                                                                  SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Klein, Michel H
TITLE OF INVENTION: ADJUVAN:
TITLE OF INVENTION: MINERAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            149 KORONKPPNKPNNDFHFEVFNFVPCSIC 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEPHONE: (416) 595-1163
TELEFAX: (416) 595-1163
TELEX: 065-24567 SIMBAS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Stewart, Michael REGISTRATION NUMBER: 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: FILING DATE: 06-JA
            TYPE: amino acid
STRANDEDNESS: sir
                                                                                                                                                                        NAME: Stewart, Michael REGISTRATION NUMBER: 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRANDEDNESS:
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ropology:
                                                 LENGTH:
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Ontario
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                                                26 amino acids
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linear
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            single
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                                                                                                                                                                                                                                                                                              Release #1.0, Version #1.30
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Pred. No. 2
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                                                                                                                                                                                                                                                                                                                 Sequence 8, Application US/08793792
Patent No. 6077511
GENERAL IMPORMATION:
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Best Local
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Best Local Similarity
Matches 19; Conser
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                               APPLICANT:
TITLE OF INVENTION: A
TITLE OF INVENTION: G
TITLE OF INVENTION: G
NUMBER OF SEQUENCES:
               CLASSIFICATION: 514
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 32 amino acids
TYPE: amino acid
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                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
LENGTH: 37 amino acids
TYPE: amino acid
STRANDEDNESS: single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: Ant TITLE OF INVENTION: G-F TITLE OF INVENTION: of NUMBER OF SEQUENCES: 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: FILING DATE:
                                                                                                   APPLICATION NUMBER: FILING DATE:
 STRANDEDNESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2, Application US/08793792 6077511
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
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single
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                                                                                                                                                                                                                                                  Antigenic peptides derived from the G-protein of RSV for type- and subtype-specific diagnosis of respiratory syncytial virus (RSV) infection.
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                                                                                                                                                                                                                                      13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     68.0%; Score 115; DB 3; 95.0%; Pred. No. 6.6e-10;
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                                                                                                                   US/08/793,792
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US-08-793-792-7
; Sequence 7, Application US/08793792
; Patent No. 6077511
; GENERAL INFORMATION:
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; HYPOTHETICAL: NO
US-08-793-792-4
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Best Local S
Matches 19
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Patent No. 6077511
GENERAL INFORMATION:
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches , 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
LENGTH: 28 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INFORMATION FOR SEQ ID NO:
                                                                                                                                                         TITLE OF INVENTION: A
TITLE OF INVENTION: C
TITLE OF INVENTION: C
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: linear MOLECULE TYPE: peptide HYPOTHETICAL: NO
                             COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOTTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/793,792
                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                  APPLICANT:
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les 19; Conserv
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CLASSIFICATION: 514
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                                                                                                                                                                        Antigenic peptides derived from the G-protein of RSV for type- and subtype-specific diagnosis of respiratory syncytial virus (RSV) infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Antigenic peptides derived from the G-protein of RSV for type- and subtype-specific diagnosis of respiratory syncytial virus (RSV) infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  64.5%;
100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     67.5%; Score 114; DB 3; 100.0%; Pred. No. 7.8e-10; tive 0; Mismatches 0;
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; Pred. No. 3.
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3.5e-09;
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STRANDEDNESS:
TOPOLOGY: line
MOLECULE TYPE: F
HYPOTHETICAL: NC
US-08-793-792-11
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US-08-793-792-11
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                                                                                                                                                                                                                 RESULT 15
US-08-793-792-3
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INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
LENGTH: 37 amino acids
TYPE: amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 85.0
Matches 17; Conservative
                                                                                                                                                                              Sequence 3, Application US/08793792 Patent No. 6077511
                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity Matches 17; Conserv
                                                                                                                                                                                                                                                                                                                                                                                            Query Match
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SEQUENCE CHARACTERISTICS:
TITLE OF INVENTION: Antigenic pepti
TITLE OF INVENTION: G-protein of RS
TITLE OF INVENTION: of respiratory
NUMBER OF SEQUENCES: 13
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                           GENERAL INFO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: PC DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION NUMBER: US/08/793,792
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: linear MOLECULE TYPE: peptide HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: Antigenic peptides derived from the TITLE OF INVENTION: G-protein of RSV for type- and subtype-specific diagnosis TITLE OF INVENTION: of respiratory syncytial virus (RSV) infection. NUMBER OF SEQUENCES: 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 32 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    10 KPNNDFHFEVFNFVPCSICG 29
                                                                                                                                                                                                                                                                                     FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 KPKDDYHFEVFNFVPCSICG 20
                                                                                                                                                              INFORMATION:
                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                : peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      62.7%;
85.0%;
                                                                                                                                                                                                                                                                                                                                                                            62.7%;
85.0%;
                                                                                      Antigenic peptides derived from the G-protein of RSV for type- and subtype-specific diagnosis of respiratory syncytial virus (RSV) infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            11:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2
                                                                                                                                                                                                                                                                                                                                                           2;
                                                                                                                                                                                                                                                                                                                                                                            Score 106; DB 3; Pred. No. 1.2e-08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 106; DB 3; Pred. No. 1.1e-08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
                                                                                                                                                                                                                                                                                                                                                           Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 32
                                                                                                                                                                                                                                                                                                                                                                                           Length 37;
                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0
                                                                                                                                                                                                                                                                                                                                                           0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0;
                                                                                                                                                                                                                                                                                                                                                           0;
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TOPOLOGY: linear

MOLECULE TYPE: peptide
HYPOTHETICAL: NO
US-08-793-792-3
 В
                    Q
                                                       Query Match 59.8%;
Best Local Similarity 84.2%;
                                                                  Query Match
                                             Matches
                                                                                                                                                                                  CLASSIFICATION: 514
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                             CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/793.700
FILING DATE:
CLASST
                                                                                                                                                LENGTH: 28 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                        LENGTH:
                       11 PNNDFHFEVFNFVPCSICG 29
16;
                                                                                                                                  linear
                                              Conservative
                                             2;
                                                        Score 101; DB 3; Pred. No. 4.7e-08;
                                              Mismatches
                                                                   Length 28;
                                              Indels
                                              0;
                                             Gaps
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